

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/922,488

DATE: 08/13/2001
TIME: 11:25:00

Input Set : A:\0054.txt
Output Set: N:\CRF3\08132001\I922488.raw

4 <110> APPLICANT: Thayer, Edward C.
5 Webster, Philippa J.
7 <120> TITLE OF INVENTION: Human Secreted Protein, Zzp1
9 <130> FILE REFERENCE: 00-54

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/922,488

C--> 11 <141> CURRENT FILING DATE: 2001-08-03

11 <150> PRIOR APPLICATION NUMBER: 60/222,814

12 <151> PRIOR FILING DATE: 2000-08-04

14 <150> PRIOR APPLICATION NUMBER: 60/260,512

15 <151> PRIOR FILING DATE: 2001-01-09

17 <160> NUMBER OF SEQ ID NOS: 5

19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 1908

23 <212> TYPE: DNA

24 <213> ORGANISM: Homo sapiens

26 <220> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (1)...(1908)

30 <400> SEQUENCE: 1

31 atg gca gga ggc tca gcc acg acc tgg ggt tac cct gtg gcc ctg cta 48

32 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu

33 1 5 10 15

35 ctg ctg gtt gcc acc ctg ggg ctg ggt agg tgg ctc cag ccc gac cca 96

36 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro

37 20 25 30

39 ggc ctc cgg cac agc tac gac tgt ggg atc aag gga atg cag ctg ctg 144

40 Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu

41 35 40 45

44 gtg ttc ccc agg cca ggc cag act ctc cgc ttc aag gtg gtg gat gaa 192

45 Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu

46 50 55 60

48 ttt ggg aac cga ttt gat gtc aac aac tgc tcc atc tgc tac cac tgg 240

49 Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp

50 65 70 75 80

52 gtc acc tcc agg ccg cag gag cct gca gtc ttc tcg gcc gat tac aga 288

53 Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg

54 85 90 95

56 ggc tgc cac gtg ctg gag aag gat ggg cgt ttc cac ctg agg gtg ttc 336

57 Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe

58 100 105 110

60 atg gag gct gtg ctg ccc aat ggt cgt gtg gat gtg gca caa gac gct 384

61 Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala

62 115 120 125

64 act ctg atc tgt ccc aaa cct gac ccc tcc cgg act ctg gac tcc cag 432

65 Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln

66 130 135 140

ENTERED

6
P-6

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68	ctg	gca	cca	ccc	gcc	atg	ttc	tct	gtc	tca	acc	cca	caa	acc	ctt	tcc	480
69	Leu	Ala	Pro	Pro	Ala	Met	Phe	Ser	Val	Ser	Thr	Pro	Gln	Thr	Leu	Ser	
70	145					150				155						160	
72	ttc	ctc	ccc	acc	tct	ggc	cat	acc	tcc	caa	ggc	tct	ggc	cat	gcc	ttt	528
73	Phe	Leu	Pro	Thr	Ser	Gly	His	Thr	Ser	Gln	Gly	Ser	Gly	His	Ala	Phe	
74						165				170						175	
76	ccc	agc	cca	ctg	gac	cca	ggg	cac	agc	tct	gtc	cac	cca	acc	cct	gct	576
77	Pro	Ser	Pro	Leu	Asp	Pro	Gly	His	Ser	Ser	Val	His	Pro	Thr	Pro	Ala	
78						180				185						190	
80	tta	cca	tcc	cct	gga	cct	gga	acc	ctc	gcc	acc	ctg	gct	caa	ccc		624
81	Leu	Pro	Ser	Pro	Gly	Pro	Gly	Pro	Thr	Leu	Ala	Thr	Leu	Ala	Gln	Pro	
82						195				200						205	
84	cac	tgg	ggc	acc	ttg	gaa	cac	tgg	gat	gtg	aac	aaa	cga	gat	tac	ata	672
85	His	Trp	Gly	Thr	Leu	Glu	His	Trp	Asp	Val	Asn	Lys	Arg	Asp	Tyr	Ile	
86						210				215						220	
88	ggt	acc	cac	ctg	agc	cag	gag	cag	tgc	cag	gtg	gcc	tca	ggg	cac	ctc	720
89	Gly	Thr	His	Leu	Ser	Gln	Glu	Gln	Cys	Gln	Val	Ala	Ser	Gly	His	Leu	
90						225				230						240	
92	ccc	tgc	atc	gtg	aga	aga	act	tca	aaa	gaa	gcc	tgt	cag	cag	gct	ggc	768
93	Pro	Cys	Ile	Val	Arg	Arg	Thr	Ser	Lys	Glu	Ala	Cys	Gln	Gln	Ala	Gly	
94						245				250						255	
96	tgc	tgc	tat	gac	aac	acc	aga	gag	gtt	ccc	tgt	tac	tat	ggc	aac	aca	816
97	Cys	Cys	Tyr	Asp	Asn	Thr	Arg	Glu	Val	Pro	Cys	Tyr	Tyr	Gly	Asn	Thr	
98						260				265						270	
100	gct	act	gtc	cag	tgc	ttc	aga	gat	ggc	tac	ttc	gtc	ctc	gta	gtg	tcc	864
101	Ala	Thr	Val	Gln	Cys	Phe	Arg	Asp	Gly	Tyr	Phe	Val	Leu	Val	Val	Ser	
102						275				280						285	
104	caa	gaa	atg	gcc	ttg	aca	cac	agg	atc	aca	ctg	gcc	aac	atc	cac	ctg	912
105	Gln	Glu	Met	Ala	Leu	Thr	His	Arg	Ile	Thr	Leu	Ala	Asn	Ile	His	Leu	
106						290				295						300	
108	gcc	tat	gcc	ccc	acc	agc	tgc	tcc	cca	aca	cag	cac	acg	gaa	gct	ttc	960
109	Ala	Tyr	Ala	Pro	Thr	Ser	Cys	Ser	Pro	Thr	Gln	His	Thr	Glu	Ala	Phe	
110						305				310						320	
112	gtg	gtc	ttc	tac	ttc	cct	ctc	acc	cac	tgt	gga	acc	aca	atg	cag	gtg	1008
113	Val	Val	Phe	Tyr	Phe	Pro	Leu	Thr	His	Cys	Gly	Thr	Thr	Met	Gln	Val	
114						325				330						335	
116	gct	ggc	gac	cag	ctc	atc	tat	gag	aac	tgg	ctg	gtg	tct	ggc	atc	cac	1056
117	Ala	Gly	Asp	Gln	Leu	Ile	Tyr	Glu	Asn	Trp	Leu	Val	Ser	Gly	Ile	His	
118						340				345						350	
120	atc	caa	aag	ggg	cca	cag	ggt	tcc	atc	acg	cg	gac	agc	acc	ttc	cag	1104
121	Ile	Gln	Lys	Gly	Pro	Gln	Gly	Ser	Ile	Thr	Arg	Asp	Ser	Thr	Phe	Gln	
122						355				360						365	
124	ctt	cat	gtg	cgc	tgt	gtc	ttc	aac	gcc	agt	gac	ttc	ctg	ccc	att	cag	1152
125	Leu	His	Val	Arg	Cys	Val	Phe	Asn	Ala	Ser	Asp	Phe	Leu	Pro	Ile	Gln	
126						370				375						380	
129	gca	tcc	att	ttc	cca	ccc	cca	tcg	cct	gct	cct	atg	acc	cag	ccc	ggc	1200
130	Ala	Ser	Ile	Phe	Pro	Pro	Pro	Ser	Pro	Ala	Pro	Met	Thr	Gln	Pro	Gly	
131						385				390						400	
133	ccc	ctg	cgg	ctt	gag	ctg	cgg	att	gcc	aaa	gac	gag	acc	tgc	agc	tgc	1248

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134	Pro	Leu	Arg	Leu	Glu	Leu	Arg	Ile	Ala	Lys	Asp	Glu	Thr	Cys	Ser	Ser
135				405												415
137	tac	tat	ggg	gag	gat	gac	tat	ccc	atc	gtg	agg	ctg	ctc	cga	gaa	cca
138	Tyr	Tyr	Gly	Glu	Asp	Asp	Tyr	Pro	Ile	Val	Arg	Leu	Leu	Arg	Glu	Pro
139				420												430
141	gtc	cat	gtg	gag	gtc	cgg	ctt	ctg	cag	agg	aca	gac	ccc	aac	ctg	gtc
142	Val	His	Val	Glu	Val	Arg	Leu	Leu	Gln	Arg	Thr	Asp	Pro	Asn	Leu	Val
143				435												445
145	ctg	ctg	ctg	cac	cag	tgc	tgg	ggc	gct	ccc	agt	gcc	aac	ccc	ttc	cag
146	Leu	Leu	Leu	His	Gln	Cys	Trp	Gly	Ala	Pro	Ser	Ala	Asn	Pro	Phe	Gln
147				450												460
149	cag	ccc	cag	tgg	ccc	atc	ctg	tca	gac	ggc	tgc	cct	ttc	aag	ggc	gac
150	Gln	Pro	Gln	Trp	Pro	Ile	Leu	Ser	Asp	Gly	Cys	Pro	Phe	Lys	Gly	Asp
151	465					470					475					480
153	agc	tac	aga	acc	caa	atg	gta	gcc	ttg	gac	ggg	gcc	aca	cct	ttc	cag
154	Ser	Tyr	Arg	Thr	Gln	Met	Val	Ala	Leu	Asp	Gly	Ala	Thr	Pro	Phe	Gln
155						485					490					495
157	tgc	cac	tac	cag	cga	ttc	act	gtt	gct	acc	ttc	gcc	ctc	ctg	gac	tca
158	Ser	His	Tyr	Gln	Arg	Phe	Thr	Val	Ala	Thr	Phe	Ala	Leu	Leu	Asp	Ser
159						500					505					510
161	ggc	tcc	cag	aga	gcc	ctc	aga	gga	ctg	gtt	tac	ttg	ttc	tgc	agc	acc
162	Gly	Ser	Gln	Arg	Ala	Leu	Arg	Gly	Leu	Val	Tyr	Leu	Phe	Cys	Ser	Thr
163						515					520					525
165	tct	gcc	tgc	cac	acc	tca	ggg	ctg	gag	act	tgc	tcc	act	gca	tgt	agc
166	Ser	Ala	Cys	His	Thr	Ser	Gly	Leu	Glu	Thr	Cys	Ser	Thr	Ala	Cys	Ser
167						530					535					540
169	act	ggc	act	aca	aga	cag	cga	cga	tcc	tca	ggt	cac	cgt	aat	gac	act
170	Thr	Gly	Thr	Arg	Gln	Arg	Arg	Ser	Ser	Gly	His	Arg	Asn	Asp	Thr	
171	545						550				555					560
173	gcc	agg	ccc	cag	gac	atc	gtg	agc	tct	ccg	ggg	cca	gtg	ggc	ttt	gag
174	Ala	Arg	Pro	Gln	Asp	Ile	Val	Ser	Ser	Pro	Gly	Pro	Val	Gly	Phe	Glu
175							565				570					575
177	gat	tct	tat	ggg	cag	gag	ccc	aca	ctt	ggg	ccc	aca	gac	tcc	aat	ggg
178	Asp	Ser	Tyr	Gly	Gln	Glu	Pro	Thr	Leu	Gly	Pro	Thr	Asp	Ser	Asn	Gly
179							580				585					590
181	aac	tcc	agc	ctg	aga	cct	ctc	ctt	tgg	gct	gtc	ctt	ttg	ctg	cca	gct
182	Asn	Ser	Ser	Leu	Arg	Pro	Leu	Leu	Trp	Ala	Val	Leu	Leu	Pro	Ala	
183							595				600					605
185	gtt	gcc	ctg	gtc	ctt	ggg	ttt	ggt	gtc	ttt	gtg	ggc	ctg	agc	cag	acc
186	Val	Ala	Leu	Val	Leu	Gly	Phe	Gly	Val	Phe	Val	Gly	Leu	Ser	Gln	Thr
187							610				615					620
189	tgg	gcc	cag	aag	ctc	tgg	gaa	agc	aac	aga	cag	tga				
190	Trp	Ala	Gln	Lys	Leu	Trp	Glu	Ser	Asn	Arg	Gln	*				
191	625					630					635					
194	<210>	SEQ ID NO:	2													
195	<211>	LENGTH:	635													
196	<212>	TYPE:	PRT													
197	<213>	ORGANISM:	Homo sapiens													
199	<400>	SEQUENCE:	2													

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200 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu
 201 1 5 10 15
 202 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
 203 20 25 30
 204 Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
 205 35 40 45
 206 Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
 207 50 55 60
 208 Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
 209 65 70 75 80
 210 Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
 211 85 90 95
 212 Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
 213 100 105 110
 215 Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
 216 115 120 125
 217 Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
 218 130 135 140
 219 Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
 220 145 150 155 160
 221 Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
 222 165 170 175
 223 Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
 224 180 185 190
 225 Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
 226 195 200 205
 227 His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
 228 210 215 220
 229 Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu
 230 225 230 235 240
 231 Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
 232 245 250 255
 233 Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
 234 260 265 270
 235 Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
 236 275 280 285
 237 Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
 238 290 295 300
 239 Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
 240 305 310 315 320
 241 Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
 242 325 330 335
 243 Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
 244 340 345 350
 245 Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
 246 355 360 365
 247 Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
 248 370 375 380
 249 Ala Ser Ile Phe Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly

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250	385	390	395	400
251	Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser			
252		405	410	415
253	Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro			
254		420	425	430
255	Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val			
256		435	440	445
258	Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln			
259		450	455	460
260	Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp			
261		465	470	475
262	Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln			
263		485	490	495
264	Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser			
265		500	505	510
266	Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr			
267		515	520	525
268	Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser			
269		530	535	540
270	Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr			
271		545	550	555
272	Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu			
273		565	570	575
274	Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly			
275		580	585	590
276	Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala			
277		595	600	605
278	Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr			
279		610	615	620
280	Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln			
281		625	630	635
284	<210> SEQ ID NO: 3			
285	<211> LENGTH: 1905			
286	<212> TYPE: DNA			
287	<213> ORGANISM: Artificial Sequence			
289	<220> FEATURE:			
290	<223> OTHER INFORMATION: degenerate nucleotide sequence			✓
292	<221> NAME/KEY: misc_feature			
293	<222> LOCATION: 6, 9, 12, 15, 18, 21, 24, 30, 36, 39, 42, 45, 48, 51, 54,			
294		57, 60, 63, 66, 69, 72, 75, 78, 84, 90, 96, 99, 102, 105,		
295		111, 123, 132, 141, 144, 147, 153, 156, 159, 162, 168, 171,		
296		174, 183, 186, 198, 204, 213, 225, 243, 246, 249, 252		
297	<223> OTHER INFORMATION: n = A,T,C or G			
299	<221> NAME/KEY: misc_feature			
300	<222> LOCATION: 255, 264, 267, 270, 276, 279, 288, 291, 300, 303, 315, 318,			
301		327, 330, 333, 345, 348, 351, 354, 360, 363, 366, 372, 375,		
302		384, 387, 390, 399, 405, 411, 414, 417, 420, 423, 429, 435,		
303		438, 441, 444, 447, 456, 459, 462, 465, 468, 474, 477		
304	<223> OTHER INFORMATION: n = A,T,C or G			

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3